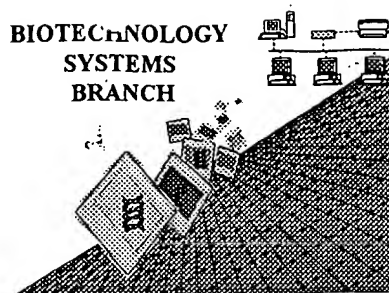


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/900,038
Source: OIPe
Date Processed by STIC: 7/24/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/900,038

DATE: 07/24/2001

TIME: 11:10:29

Input Set : A:\766.53 CRF.txt

Output Set: N:\CRF3\07242001\I900038.raw

pg 1-3
 Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
 5 <120> TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the same
 7 <130> FILE REFERENCE: 11328
 9 <140> CURRENT APPLICATION NUMBER: US/09/900,038
 9 <141> CURRENT FILING DATE: 2001-07-09
 9 <150> PRIOR APPLICATION NUMBER: JP 2001-392
 W--> 10 <151> PRIOR FILING DATE: 2001-1-5 *2001-01-05 ← use this date format*
 12 <160> NUMBER OF SEQ ID NOS: 8
 14 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

16 <210> SEQ ID NO: 1
 17 <211> LENGTH: *← mandatory response needed - 3/3 shown (p2)*
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Streptococcus agalactiae Type Ib
 20 <400> SEQUENCE: 1
 21 Met Asn Tyr Ser Ile Ile Met Ser Val Tyr Asn Glu Pro Leu Asn Tyr
 22 1 5 10 15
 24 Val Arg Asp Ser Val Glu Ser Ile Leu Asn Gln Thr Leu Thr Asp Phe
 25 20 25 30
 27 Glu Phe Ile Ile Val Ile Asp Asn Pro Ser Arg Gly Asp Leu Lys Gln
 28 35 40 45
 30 Phe Leu Thr Glu Tyr Ser Val Asp Asn Arg Ile Lys Ile Leu Leu
 31 50 55 60
 33 Asn Glu Glu Asn Ile Gly Leu Ala Ser Ser Leu Asn Lys Ala Val Lys
 34 65 70 75 80
 36 Ile Ser Lys Gly Glu Tyr Ile Phe Arg Met Asp Ala Asp Asp Ile Ser
 37 85 90 95
 39 Tyr Pro Ser Arg Phe Asp Lys Gln Ile Arg Phe Met Glu Glu Asn Ser
 40 100 105 110
 42 Leu Asp Phe Ser Ala Thr Leu Ile Glu Leu Ile Asp Gln Lys Gly Asn
 43 115 120 125
 45 Leu Val Tyr Lys Lys Gln Arg Glu Ser Asn Lys Ile Tyr Leu Thr Asn Asp
 46 130 135 140
 48 Ile Arg Lys Met Leu Leu Asn Arg Ser Ile Leu Ala His Pro Thr Trp
 49 145 150 155 160
 51 Cys Val Lys Lys Lys Val Phe Asp Lys Leu Met Gly Tyr Arg Asp Leu
 52 165 170 175
 54 Val Pro Val Glu Asp Tyr Asp Phe Ala Ile Arg Gly Ala Leu Ala Asp
 55 180 185 190
 57 Phe Lys Ile Gly Leu Leu Asn Lys Val Leu Leu Gln Tyr Arg Leu Asn
 58 195 200 205
 60 Glu Asn Gly Ile Ser Gln Thr Asn Lys Phe Lys Gln Tyr Ile Tyr Ser
 61 210 215 220
 63 Ala Ile Leu Gln Asp Phe Tyr Lys Glu Lys Ser Tyr Ile Asp Ile Thr

RAW SEQUENCE LISTING

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Input Set : A:\766.53 CRF.txt

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64 225 230 235 240
 66 Lys Ile Thr Asn Tyr Phe Gln Glu Tyr Val Ile Lys Lys Arg Tyr Thr
 67 245 250 255
 69 Gln Gln Glu Leu Ser Lys Tyr Phe Glu Leu Lys Ser Thr Pro Ser Ile
 70 260 265 270
 72 Thr Ile Arg Lys Leu Tyr Ile Cys Leu Tyr Leu Tyr Phe Lys Ser Pro
 73 275 280 285
 75 Leu Val Arg Arg Leu Leu Ile Asn Asp Ile Asn Ile Leu Val Leu Lys
 76 290 295 300
 78 Leu Phe Gly Gly Glu Lys Gln Ser Asp
 E--> 79 305 310 ~~315~~ *number the amino acids under every 5 = amino acids*
 81 <210> SEQ ID NO: 2
 82 <211> LENGTH: *same even 939 shown (p.3)*
 83 <212> TYPE: DNA
 84 <213> ORGANISM: Streptococcus agalactiae Type Ib
 85 <400> SEQUENCE: 2
 86 atg aat tat agt atc att atg tcg gta tat aat gag cct tta aat tat 48
 87 Met Asn Tyr Ser Ile Ile Met Ser Val Tyr Asn Glu Pro Leu Asn Tyr
 88 1 5 10 15
 90 gtg aga gat tca gta gaa tct ata tta aat caa acg ctt act gat ttt 96
 91 Val Arg Asp Ser Val Glu Ser Ile Leu Asn Gln Thr Leu Thr Asp Phe
 92 20 25 30
 94 gag ttc ata att gtc att gat aat cca agt aga ggt gat tta aag caa 144
 95 Glu Phe Ile Ile Val Ile Asp Asn Pro Ser Arg Gly Asp Leu Lys Gln
 96 35 40 45
 98 ttc tta aca gaa tat tca gtt gta gat aat aga ata aaa atc ttg ctt 192
 99 Phe Leu Thr Glu Tyr Ser Val Val Asp Asn Arg Ile Lys Ile Leu Leu
 100 50 55 60
 102 aat gaa gaa aat att ggt tta gca tca agt ttg aac aaa gcg gtg aaa 240
 103 Asn Glu Glu Asn Ile Gly Leu Ala Ser Ser Leu Asn Lys Ala Val Lys
 104 65 70 75 80
 106 att tct aag gga gaa tat att ttt aga atg gat gct gat gat att tca 288
 107 Ile Ser Lys Gly Glu Tyr Ile Phe Arg Met Asp Ala Asp Asp Ile Ser
 108 85 90 95
 110 tat cca agt aga ttt gat aag caa att cgt ttt atg gag gaa aat tca 336
 111 Tyr Pro Ser Arg Phe Asp Lys Gln Ile Arg Phe Met Glu Glu Asn Ser
 112 100 105 110
 114 ttg gat ttc tca gca act cta ata gaa ttg ata gac caa aaa gga aat 384
 115 Leu Asp Phe Ser Ala Thr Leu Ile Glu Leu Ile Asp Gln Lys Gly Asn
 116 115 120 125
 118 tta gta tat aaa caa cga gaa agt aat aaa ata tac tta act aat gat 432
 119 Leu Val Tyr Lys Gln Arg Glu Ser Asn Lys Ile Tyr Leu Thr Asn Asp
 120 130 135 140
 122 ata cgg aag atg tta ttg aat aga tct ata ctt gcc cac cca acg tgg 480
 123 Ile Arg Lys Met Leu Leu Asn Arg Ser Ile Leu Ala His Pro Thr Trp
 124 145 150 155 160
 126 tgc gta aaa aag aaa gtt ttc gat aag tta atg gga tat aga gat tta 528
 127 Cys Val Lys Lys Lys Val Phe Asp Lys Leu Met Gly Tyr Arg Asp Leu
 128 165 170 175

RAW SEQUENCE LISTING

DATE: 07/24/2001

PATENT APPLICATION: US/09/900,038

TIME: 11:10:29

Input Set : A:\766.53 CRF.txt

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```

130  gta cct gtt gaa gat tat gat ttt gca ata aga gga gct ctg gct gat   576
131  Val Pro Val Glu Asp Tyr Asp Phe Ala Ile Arg Gly Ala Leu Ala Asp
132              180                      185                      190
134  ttc aaa atc ggc tta ctc aat aaa gta ctt tta cag tat aga tta aac   624
135  Phe Lys Ile Gly Leu Leu Asn Lys Val Leu Leu Gln Tyr Arg Leu Asn
136              195                      200                      205
138  gag aat gga ata tca caa acc aat aag ttt aag caa tat att tac tca   672
139  Glu Asn Gly Ile Ser Gln Thr Asn Lys Phe Lys Gln Tyr Ile Tyr Ser
140              210                      215                      220
142  gct att tta caa gat ttt tat aaa gaa aaa tct tat att gat atc aca   720
143  Ala Ile Leu Gln Asp Phe Tyr Lys Glu Lys Ser Tyr Ile Asp Ile Thr
144  225              230              235              240
146  aaa att act aat tac ttt caa gag tat gtg ata aag aaa cgc tat act   768
147  Lys Ile Thr Asn Tyr Phe Gln Glu Tyr Val Ile Lys Lys Arg Tyr Thr
148              245              250              255
150  cag caa gag ctc tct aaa tat ttt gag cta aaa tct acc cct agt att   816
151  Gln Gln Glu Leu Ser Lys Tyr Phe Glu Leu Lys Ser Thr Pro Ser Ile
152              260              265              270
154  act att aga aaa cta tat att tgt tta tat tta tac ttt aag tct ccc   864
155  Thr Ile Arg Lys Leu Tyr Ile Cys Leu Tyr Leu Tyr Phe Lys Ser Pro
156              275              280              285
158  ttg gtt agg agg tta tta ata aat gat att aat att tta gta ctg aaa   912
159  Leu Val Arg Arg Leu Leu Ile Asn Asp Ile Asn Ile Leu Val Leu Lys
160              290              295              300
162  ttg ttt gga gga gag aaa caa agt gac                               939
163  Leu Phe Gly Gly Glu Lys Gln Ser Asp
G--> 164  305              310
730 <210> SEQ ID NO: 8
731 <211> LENGTH: 32
732 <212> TYPE: DNA
733 <213> ORGANISM: Artificial Sequence
G--> 734 <220> FEATURE:
735 <223> OTHER INFORMATION: Synthetic DNA
E--> 736 <400> SEQUENCE: 8 (insert)
737  ccggaattcg aaaaggtaaa gtgtctccga aa                               32

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/900,038

DATE: 07/24/2001

TIME: 11:10:30

Input Set : A:\766.53 CRF.txt

Output Set: N:\CRF3\07242001\I900038.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:20 M:283 W: Missing Blank Line separator, <400> field identifier
L:79 M:252 E: No. of Seq. differs, <211>LENGTH:Input:0 Found:313 SEQ:1
L:85 M:283 W: Missing Blank Line separator, <400> field identifier
L:164 M:252 E: No. of Seq. differs, <211>LENGTH:Input:0 Found:939 SEQ:2
L:693 M:283 W: Missing Blank Line separator, <220> field identifier
L:695 M:283 W: Missing Blank Line separator, <400> field identifier
L:704 M:283 W: Missing Blank Line separator, <220> field identifier
L:706 M:283 W: Missing Blank Line separator, <400> field identifier
L:714 M:283 W: Missing Blank Line separator, <220> field identifier
L:716 M:283 W: Missing Blank Line separator, <400> field identifier
L:724 M:283 W: Missing Blank Line separator, <220> field identifier
L:726 M:283 W: Missing Blank Line separator, <400> field identifier
L:734 M:283 W: Missing Blank Line separator, <220> field identifier
L:736 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:8 differs:7
L:736 M:283 W: Missing Blank Line separator, <400> field identifier